

OM protein - protein search, using sw model

Run on: May 19, 2004, 16:52:51 ; Search time 63.75 Seconds  
(without alignments)  
66.482 Million cell updates/sec

Title: US-10-034-974-7

Perfect score: 104

Sequence: 1 WKACPGEDWLFCWGS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: geneseqp1980s.\*

2: geneseqp1990s.\*

3: geneseqp2000s.\*

4: geneseqp2001s.\*

5: geneseqp2002s.\*

6: geneseqp2003as.\*

7: geneseqp2003bs.\*

8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	15	5 AAE26735	Aae26735 Fibrin bi
2	73	70.2	15	5 AAE26758	Aae26758 Fibrin bi
3	70	67.3	15	5 AAE26762	Aae26762 Fibrin bi
4	66	63.5	15	5 AAE26733	Aae26733 Fibrin bi
5	66	63.5	19	5 AAE26744	Aae26744 Slow diss
6	66	63.5	19	5 AAE26745	Aae26745 Slow diss
7	66	63.5	19	5 AAE26743	Aae26743 Slow diss
8	63	60.6	9	5 AAE26753	Aae26753 Fibrin bi
9	63	60.6	15	5 AAE26732	Aae26732 Fibrin bi

10	60	57.7	15	5 AAE26731	Aae26731 Fibrin bi
11	57	54.8	15	5 AAE26764	Aae26764 Fibrin bi
12	56	53.8	15	5 AAE26765	Aae26765 Fibrin bi
13	56	53.8	15	5 AAE26766	Aae26766 Fibrin bi
14	54.5	52.4	51	4 AAE61462	Aae61462 Propionib
15	54.5	52.4	51	6 AAE57981	Aae57981 Propionib
16	53.5	51.4	4347	4 AAE59051	Aae59051 Drosophila
17	51	49.0	9	5 AAE26777	Aae26777 Fibrin bi
18	51	49.0	9	5 AAE26778	Aae26778 Fibrin bi
19	51	49.0	15	5 AAE26761	Aae26761 Fibrin bi
20	51	49.0	33	2 AAE40294	Aae40294 Human con
21	51	49.0	255	5 AAE45903	Aae45903 Human Bly
22	50.5	48.6	34	2 AAE06189	Aae06189 Anti-angi
23	50	48.1	9	5 AAE26780	Aae26780 Fibrin bi
24	50	48.1	15	5 AAE26734	Aae26734 Fibrin bi
25	50	48.1	19	5 AAE26746	Aae26746 Slow diss
26	50	48.1	19	5 AAE26748	Aae26748 Slow diss
27	50	48.1	19	5 AAE26747	Aae26747 Slow diss
28	48	46.2	9	5 AAE26774	Aae26774 Fibrin bi
29	48	46.2	270	4 AAE30149	Aae30149 Novel hum
30	47	45.2	93	4 AAE24468	Aae24468 Novel hum
31	46.5	44.7	85	5 AAE43519	Aae43519 Human sec
32	46	44.2	98	4 AAE50783	Aae50783 Human sec
33	46	44.2	98	6 AAE45040	Aae45040 Novel hum
34	46	44.2	98	7 AAE26520	Aae26520 Protein a
35	46	44.2	339	6 AAE23786	Aae23786 Protein e
36	46	44.2	347	3 AAE13457	Aae13457 Arabidops
37	46	44.2	347	3 AAE52967	Aae52967 Arabidops
38	46	44.2	365	3 AAE52966	Aae52966 Arabidops
39	46	44.2	365	3 AAE13456	Aae13456 Arabidops
40	46	44.2	423	3 AAE52965	Aae52965 Arabidops
41	46	44.2	423	3 AAE13455	Aae13455 Arabidops
42	46	44.2	1695	4 AAE83975	Aae83975 Amino aci
43	45.5	43.8	169	2 AAE60559	Aae60558 Human nor
44	45.5	43.8	289	4 AAE93469	Aae93469 Human pro
45	45.5	43.8	580	4 AAE16207	Aae16207 Human nov

#### ALIGNMENTS

RESULT 1  
AAE26735  
ID AAE26735 standard; peptide; 15 AA.  
XX  
XX  
AC AAE26735;  
XX  
DT 13-DEC-2002 (first entry)  
DE Fibrin binding peptide #6.  
XX  
KW Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;  
KW myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotrophic;  
KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;  
KW inflammatory disorder; angiogenesis; stroke; cerebroprotective.  
XX  
OS Unidentified.

XX WO20025544-A2.  
 XX 18-JUL-2002.  
 XX 21-DEC-2001; 2001WO-US049534.  
 XX 23-DEC-2000; 2000US-00747403.  
 XX (DYAX-) DVAX CORP.  
 XX Wescott CR, Beltzer JP, Sato AK;  
 XX WPI; 2002-666875/71.  
 XX Novel synthetic fibrin-binding moiety, useful for detecting, imaging or  
 PT localizing fibrin-containing clots by magnetic resonance imaging,  
 PT radioimaging and for treating diseases involving thrombus formation e.g.  
 PT stroke.  
 XX Claim 10; Page 57; 69pp; English.  
 XX The invention relates to a synthetic fibrin binding group having affinity  
 CC for fibrin. The invention is useful for detecting fibrin in a mammalian  
 CC subject which involves (a) detectably labelling the binding group; (b)  
 CC administering to the subject the labelled polypeptide, and (c) detecting  
 CC the labelled polypeptide in the subject. The invention is useful for  
 CC treating a disease involving thrombus formation eg. deep-vein thrombosis,  
 CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial  
 CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful  
 CC for detection, imaging and localisation of fibrin-containing clots by  
 CC magnetic resonance imaging, radioimaging and other imaging methods and  
 CC are also useful in the diagnosis and treatment of coronary conditions  
 CC where fibrin plays a role. The fibrin binding moieties are useful for  
 CC detecting and diagnosing numerous pathophysiological conditions in which fibrin plays  
 CC a role eg. peritoneal adhesions which often occur after surgery or  
 CC inflammatory and neoplastic processes and are comprised of a fibrin  
 CC network, fibroblasts, macrophages and new blood vessels; rheumatoid  
 CC arthritis, lupus or septic arthritis which often have bits of fibrin  
 CC containing tissues called rice bodies in the synovial fluid of their  
 CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in  
 CC arterioles causes turbulent blood flow resulting in stress and  
 CC destruction of red blood cells. The fibrin specific agents can also be  
 CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain  
 CC or other organs, as well as the detection of tumours, diabetic  
 CC retinopathy, early or high-risk atherosclerosis and other autoimmune and  
 CC inflammatory disorders. Fibrin specific agents also could provide both  
 CC direct or surrogate markers of disease models in which hypoxia and  
 CC angiogenesis are expected to play a role. The invention is also useful  
 CC for screening molecular libraries. The present sequence is a fibrin  
 CC binding peptide  
 XX  
 XX Sequence 15 AA;  
 Query Match 100.0%; Score 104; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKACPGEDWLFOWGS 15  
 |||||  
 Db 1 WKACPGEDWLFOWGS 15  
 Search completed: May 19, 2004, 17:05:46  
 Job time : 64.75 secs

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OM protein - protein search, using sw model

Run on: May 19, 2004, 17:07:54 ; Search time 51.875 Seconds  
(without alignments)  
80.461 Million cell updates/sec

Title: US-10-034-974-7

Perfect score: 104  
Sequence: 1 WKACPGEDWLCWGS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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RESULT 1  
US-10-034-974-7  
; Sequence 7, Application US/10034974  
; Publication No. US20030143158A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP.

#### ALIGNMENTS

1	104	100.0	15	14	US-10-034-974-7	Sequence 7, Appli
2	73	70.2	15	14	US-10-034-974-30	Sequence 30, Appl
3	70	67.3	15	14	US-10-034-974-34	Sequence 34, Appl
4	66	63.5	15	14	US-10-034-974-5	Sequence 5, Appli
5	66	63.5	19	14	US-10-034-974-15	Sequence 15, Appl
6	66	63.5	19	14	US-10-034-974-16	Sequence 16, Appl
7	66	63.5	19	14	US-10-034-974-17	Sequence 17, Appl
8	63	60.6	9	14	US-10-034-974-25	Sequence 25, Appl
9	63	60.6	15	14	US-10-034-974-4	Sequence 4, Appli
10	60	57.7	15	14	US-10-034-974-3	Sequence 3, Appli
11	57	54.8	15	14	US-10-034-974-36	Sequence 36, Appl
12	56	53.8	15	14	US-10-034-974-37	Sequence 37, Appl
13	56	53.8	15	14	US-10-034-974-38	Sequence 38, Appl
14	51	49.0	9	14	US-10-034-974-49	Sequence 49, Appl
15	51	49.0	9	14	US-10-034-974-50	Sequence 50, Appl
16	51	49.0	15	14	US-10-034-974-33	Sequence 33, Appl
17	51	49.0	25	10	US-09-880-748-1914	Sequence 1914, Ap
18	51	49.0	25	12	US-10-293-418-1914	Sequence 1914, Ap
19	50.5	48.6	34	13	US-10-036-869-15	Sequence 15, Appl
20	50	48.1	9	14	US-10-034-974-52	Sequence 52, Appl
21	50	48.1	15	14	US-10-034-974-6	Sequence 6, Appli
22	50	48.1	19	14	US-10-034-974-18	Sequence 18, Appl
23	50	48.1	19	14	US-10-034-974-19	Sequence 19, Appl
24	50	48.1	19	14	US-10-034-974-20	Sequence 20, Appl
25	49	47.1	379	14	US-10-029-386-32938	Sequence 32938, A
26	48	46.2	9	14	US-10-034-974-46	Sequence 46, Appl
27	46	44.2	65	12	US-10-424-599-194290	Sequence 194290,
28	46	44.2	98	10	US-09-933-767-736	Sequence 736, App
29	46	44.2	98	12	US-10-004-860-736	Sequence 736, App
30	46	44.2	98	14	US-10-023-282-736	Sequence 736, App
31	46	44.2	339	12	US-10-282-122A-51710	Sequence 51710, A
32	45.5	43.8	580	9	US-09-764-864-1160	Sequence 1160, Ap
33	45.5	43.8	1047	15	US-10-094-749-2629	Sequence 2629, Ap
34	45	43.3	26	14	US-10-058-053A-303	Sequence 303, App
35	45	43.3	37	14	US-10-058-053A-287	Sequence 287, App
36	45	43.3	37	14	US-10-058-053A-288	Sequence 288, App
37	45	43.3	37	14	US-10-058-053A-289	Sequence 289, App
38	45	43.3	44	12	US-10-632-983-104	Sequence 104, App
39	45	43.3	80	14	US-10-058-053A-110	Sequence 110, App
40	45	43.3	96	12	US-10-632-983-103	Sequence 103, App
41	45	43.3	101	12	US-10-424-599-144611	Sequence 144611,
42	45	43.3	109	14	US-10-058-053A-143	Sequence 143, App
43	45	43.3	110	14	US-10-058-053A-167	Sequence 167, App
44	45	43.3	110	14	US-10-058-053A-173	Sequence 173, App
45	45	43.3	494	12	US-10-425-114-65620	Sequence 65620, A

; APPLICANT: Beltzer, James P.  
; APPLICANT: Wescott, Charles R.  
; APPLICANT: Sato, Aaron K.  
; TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS  
; FILE REFERENCE: DIX-024.1 PCT; DIX-024.1 US  
; CURRENT APPLICATION NUMBER: US/10/034,974  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 09/747,403  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fibrin binding polypeptide  
US-10-034-974-7

Query Match 100.0%; Score 104; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred.No. 3.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WKACPGEDWLCWGS 15  
|||||  
Db 1 WKACPGEDWLCWGS 15

Search completed: May 19, 2004, 17:17:35  
Job time : 58.875 secs

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OM protein - protein search, using sw model

Run on: May 19, 2004, 16:59:56 ; Search time 16.875 Seconds  
(without alignments)  
85.504 Million cell updates/sec

Title: US-10-034-974-7  
Perfect score: 104  
Sequence: 1 WKACPGEDWLCWGS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	48.1	215	2 JCS114	glutathione transf
2	47	45.2	624	2 S74222	alpha-galactosidas
3	46	44.2	339	2 F97190	phenylalanyl-tRNA
4	46	44.2	423	2 G65255	CDP-diacylglycerol
5	46	44.2	423	2 T04915	CDP-diacylglycerol
6	45.5	43.8	1633	2 JCS056	polydromo 1 - chic
7	45	43.3	119	2 T46478	hypothetical prote
8	45	43.3	242	2 G83281	hypothetical prote
9	45	43.3	499	2 S28306	hypothetical prote
10	45	43.3	532	2 E69343	2-oxoacid-ferredox
11	45	43.3	579	2 D88551	protein T23G5.5 (i
12	45	43.3	615	2 T43330	catecholamine tran
13	44	42.3	217	2 S54138	probable coat prot

14 44 42.3 259 2 F36899  
15 44 42.3 259 2 S35136  
16 44 42.3 277 2 F66777  
17 44 42.3 458 2 A56055  
18 44 42.3 651 2 D86977  
19 43 41.3 292 2 G88071  
20 43 41.3 297 2 A82832  
21 43 41.3 297 2 F97609  
22 43 41.3 3036 2 T18995  
23 42.5 40.9 148 2 A86079  
24 42.5 40.9 148 2 B91232  
25 42.5 40.9 148 2 D48649  
26 42 40.4 195 2 D96341  
27 42 40.4 236 2 B70488  
28 42 40.4 346 2 T35363  
29 42 40.4 437 2 G97298  
30 42 40.4 558 2 E91170  
31 42 40.4 558 2 E86016  
32 42 40.4 590 2 A56335  
33 42 40.4 820 2 E95980  
34 42 40.4 822 2 D87325  
35 42 40.4 922 2 T23573  
36 42 40.4 943 2 S59317  
37 41.5 39.9 203 2 A53294  
38 41.5 39.9 889 2 S51465  
39 41 39.4 250 2 B72454  
40 41 39.4 292 2 A83779  
41 41 39.4 353 1 F2VF01  
42 41 39.4 429 2 T21113  
43 41 39.4 438 2 T04800  
44 41 39.4 521 2 T18896  
45 41 39.4 538 2 H70379

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OK protein - protein search, using sw model  
Run on: May 19, 2004, 16:56:57 ; Search time 12.5 Seconds  
(without alignments)  
62.484 Million cell updates/sec  
Title: US-10-034-974-7  
Perfect score: 104  
Sequence: 1 WRACPGEDWLFQWGS 15  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_42.\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES									
Result	No.	Score	Match	Length	DB	ID	Description		
1	46	44.2	339	1	SYFA_CLOAB		O97gk9 clostridium		
2	46	44.2	1199	1	Y173_HUMAN		Q14879 homo sapien		
3	45	43.3	615	1	NTDO_CAEEL		Q03614 caenorhabdi		
4	44	42.3	259	1	YMEB_LACLA		Q02151 lactococcus		
5	44	42.3	651	1	PRIA_MYCLE		Q9ccq3 mycobacteri		
6	42.5	40.9	148	1	PTVA_ECOLI		P32155 escherichia		
7	42	40.4	237	1	TRPF_PICPA		O13504 pichia past		
8	42	40.4	321	1	FCL_HUMAN		O13630 homo sapien		
9	42	40.4	346	1	VANL_STRCO		Q9xak7 streptomyce		
10	42	40.4	943	1	DIP2_YEAST		Q12220 saccharomyc		
11	41.5	39.9	889	1	RSC2_YEAST		Q06488 saccharomyc		
12	41	39.4	250	1	TDKH_AERPE		Q9y910 aeropyrum p		
13	41	39.4	254	1	PRMA_THETH		Q84bq9 thermus the		
14	41	39.4	365	1	FXH1_HUMAN		O75593 homo sapien		
15	41	39.4	413	1	WDR4_MOUSE		Q9ep82 mus musculu		
16	41	39.4	441	1	EMJ1_HUMAN		Q96a84 homo sapien		
17	41	39.4	444	1	EMJ1_MOUSE		Q91v15 mus musculu		

Search completed: May 19, 2004, 17:08:25  
Job time : 17.875 secs

18 41 39.4 465 1 GFR2\_CHICK  
19 41 39.4 687 1 C1CL\_RAT  
20 41 39.4 725 1 NC42\_MOUSE  
21 40 38.5 273 1 SCAB\_RANCA  
22 40 38.5 421 1 CDS1\_ARATH  
23 40 38.5 521 1 VENV\_DHRV1  
24 40 38.5 522 1 AOF\_ONCMY  
25 40 38.5 621 1 GLGB\_RHOMR  
26 40 38.5 655 1 PRIA\_MYCTU  
27 40 38.5 725 1 GUNG\_CLOCE  
28 40 38.5 866 1 F1BA\_HUMAN  
29 39.5 38.0 531 1 P111\_MOUSE  
30 39.5 38.0 2352 1 MORC\_SCHPO  
31 39.5 38.0 2616 1 NDL\_DROME  
32 39 37.5 62 1 VKIL\_BPP22  
33 39 37.5 106 1 YB91\_YEAST  
34 39 37.5 201 1 YMW3\_YEAST  
35 39 37.5 206 1 EBRP\_HUMAN  
36 39 37.5 398 1 GSP1\_KLEPN  
37 39 37.5 410 1 TX28\_HUMAN  
38 39 37.5 424 1 CDS1\_SOLTU  
39 39 37.5 445 1 ENV\_MLVR  
40 39 37.5 452 1 E2BG\_HUMAN  
41 39 37.5 513 1 AMY3\_SCHPO  
42 39 37.5 521 1 YF92\_MYCPN  
43 39 37.5 536 1 THIP\_ECOLI  
44 39 37.5 603 1 FOXE\_LACPL  
45 39 37.5 646 1 SCE2\_XENLA

O13157 gallus gall  
P51802 rattus norv  
P13594 mus musculu  
Q94754 rana catesb  
O04928 a phosphati  
P27427 dhori virus  
P49253 oncothrychnu  
Q93hu3 rhodothermu  
P71670 mycobacteri  
P37700 clostridium  
P02671 homo sapien  
Q8r526 mus musculu  
P98u14 schizosacch  
P98159 drosophila  
P14111 bacteriopho  
P38341 saccharomyc  
Q04772 saccharomyc  
Q9by08 homo sapien  
P15751 klebsiella  
O15462 homo sapien  
O04940 s phosphati  
P03395 friend muri  
Q9nr50 homo sapien  
O14154 schizosacch  
Q50335 mycoplasma  
P31549 escherichia  
P37063 lactobacill  
O13262 xenopus lae

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OM protein - protein search, using sw model

Run on: May 19, 2004, 16:58:07 ; Search time 45.625 Seconds  
(without alignments)  
103.732 Million cell updates/sec

Title: US-10-034-974-7

Perfect score: 104

Sequence: 1 WACPGELWFCWGS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertibrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteria:\*
- 17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB	ID	Description
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1	53.5	51.4	1952	5	Q95SN5	Q95sn5 drosophila
2	53.5	51.4	4547	5	Q9w343	Q9w343 drosophila
3	52	50.0	365	12	Q91TQ6	Q91tq6 tupaia herp
4	50	48.1	215	10	Q42706	Q42706 cocomyxa s
5	50	48.1	217	12	Q8v323	Q8v323 citrus vari
6	50	48.1	217	12	Q8v325	Q8v325 citrus vari
7	49	47.1	467	10	Q941V5	Q941v5 oryza sativ
8	48	46.2	558	11	Q8ca33	Q8ca33 mus musculu
9	47.5	45.7	144	2	Q8RQV1	Q8rqv1 bacillus gl
10	47.5	45.7	661	16	Q7UR25	Q7ur25 rhodopirell
11	47	45.2	157	11	Q8BLH8	Q8blh8 mus musculu
12	47	45.2	185	11	Q8BKJ6	Q8bkj6 mus musculu
13	47	45.2	624	3	Q92451	Q92451 trichoderma
14	46	44.2	302	16	Q7U6X7	Q7u6x7 synchococc
15	46	44.2	315	16	Q9KYU8	Q9kyu8 streptomyce
16	46	44.2	423	10	Q49639	Q49639 arabidopsis
17	46	44.2	889	16	Q82V65	Q82v65 nitrosomona
18	46	44.2	1199	4	Q8Ww29	Q8ww29 homo sapien
19	45.5	43.8	289	4	Q9NUX9	Q9nuu9 homo sapien
20	45.5	43.8	503	10	Q9M3B9	Q9m3b9 chlamydomon
21	45.5	43.8	551	5	Q9GRT8	Q9grt8 leishmania
22	45.5	43.8	605	5	Q9GYD0	Q9gyd0 leishmania
23	45.5	43.8	1047	4	Q96MS2	Q96ms2 homo sapien
24	45.5	43.8	1582	4	Q9H2T3	Q9h2t3 homo sapien
25	45.5	43.8	1602	4	Q9H2T5	Q9h2t5 homo sapien
26	45.5	43.8	1633	13	Q90941	Q90941 gallus gall
27	45.5	43.8	1634	4	Q9H314	Q9h314 homo sapien
28	45.5	43.8	1689	4	Q86U86	Q86u86 homo sapien
29	45	43.3	119	4	Q9NSV2	Q9nsv2 homo sapien
30	45	43.3	120	11	Q8C4A2	Q8c4a2 mus musculu
31	45	43.3	144	4	Q9HBQ8	Q9hbq8 homo sapien
32	45	43.3	217	12	Q66106	Q66106 citrus leaf
33	45	43.3	242	16	Q9H2T8	Q9h2t8 pseudomonas
34	45	43.3	315	16	Q8F9F7	Q8f9f7 leptospira
35	45	43.3	384	10	Q7X920	Q7x920 oryza sativ
36	45	43.3	393	16	Q8ZTM7	Q8ztm7 nitrosomona
37	45	43.3	428	10	Q9FSJ6	Q9fsj6 oryza sativ
38	45	43.3	532	17	Q29509	Q29509 archaeoglob
39	45	43.3	1053	16	Q9RKY3	Q9rk93 streptomyce
40	44.5	42.8	434	5	Q7YZS7	Q7yzs7 ciona intes
41	44	42.3	212	12	Q99HQ7	Q99hq7 tulare appl
42	44	42.3	217	12	Q8V322	Q8v322 citrus vari
43	44	42.3	217	12	Q8V321	Q8v321 citrus vari
44	44	42.3	217	12	Q8V324	Q8v324 citrus vari
45	44	42.3	217	12	Q8V326	Q8v326 citrus vari

Search completed: May 19, 2004, 17:07:46  
Job time : 47.625 secs

OM protein - protein search, using sw model

Run on: May 19, 2004, 16:52:51 ; Search time 38.25 Seconds  
(without alignments)  
66.482 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEWLF 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues  
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	9	5 AAE26753	Aae26753 Fibrin bi
2	63	100.0	15	5 AAE26735	Aae26735 Fibrin bi
3	51	81.0	9	5 AAE26777	Aae26777 Fibrin bi
4	51	81.0	9	5 AAE26778	Aae26778 Fibrin bi
5	51	81.0	15	5 AAE26762	Aae26762 Fibrin bi
6	51	81.0	15	5 AAE26761	Aae26761 Fibrin bi
7	50	79.4	9	5 AAE26780	Aae26780 Fibrin bi
8	50	79.4	15	5 AAE26764	Aae26764 Fibrin bi
9	48	76.2	9	5 AAE26774	Aae26774 Fibrin bi

10	48	76.2	15	5 AAE26758	Aae26758 Fibrin bi
11	44	69.8	9	5 AAE26751	Aae26751 Fibrin bi
12	44	69.8	15	5 AAE26733	Aae26733 Fibrin bi
13	44	69.8	19	5 AAE26744	Aae26744 Slow diss
14	44	69.8	19	5 AAE26745	Aae26745 Slow diss
15	44	69.8	19	5 AAE26743	Aae26743 Slow diss
16	42	66.7	9	5 AAE26750	Aae26750 Fibrin bi
17	42	66.7	15	5 AAE26732	Aae26732 Fibrin bi
18	42	66.7	147	4 AAU28117	AAU28117 Novel hum
19	42	66.7	314	3 AAY81361	AAY81361 Human GDP
20	42	66.7	321	2 AAY28286	AAY28286 Amino aci
21	42	66.7	321	3 AAY54116	AAY54116 A GDP-4-k
22	42	66.7	321	3 AAG007263	AAG007263 Human p53
23	42	66.7	435	4 AAU28305	AAU28305 Novel hum
24	42	66.7	595	5 ABP69754	ABP69754 Human pol
25	42	66.7	595	5 ABR82247	ABR82247 Human nuc
26	42	66.7	1165	4 ABB11946	ABB11946 Novel hum
27	41	65.1	1222	4 ABB11946	ABB11946 Human pre
28	41	65.1	1222	4 AAV79508	AAV79508 Human pro
29	40.5	64.3	4547	4 ABB59051	ABB59051 Drosophill
30	40	63.5	9	5 AAE26752	Aae26752 Fibrin bi
31	40	63.5	15	5 AAE26734	Aae26734 Fibrin bi
32	40	63.5	19	5 AAE26746	Aae26746 Slow diss
33	40	63.5	19	5 AAE26748	Aae26748 Slow diss
34	40	63.5	19	5 AAE26747	Aae26747 Slow diss
35	40	63.5	21	5 ABP47152	ABP47152 Human Bly
36	40	63.5	121	4 AAU11054	AAU11054 Human pol
37	40	63.5	255	5 ABP45903	ABP45903 Human Bly
38	40	63.5	316	4 ABG22448	ABG22448 Novel hum
39	40	63.5	943	6 ABR53214	ABR53214 Protein s
40	40	63.5	1658	4 ABG06029	ABG06029 Novel hum
41	39	61.9	60	4 AAU39512	AAU39512 Propionib
42	39	61.9	60	6 ABM36031	ABM36031 Propionib
43	39	61.9	166	3 ABA43631	ABA43631 Human can
44	39	61.9	194	5 ABB80581	ABB80581 Human seg
45	39	61.9	200	4 ABG04658	ABG04658 Novel hum

#### ALIGNMENTS

RESULT 1  
AAE26753  
ID AAE26753 standard; peptide; 9 AA.  
XX  
AC AAE26753;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Fibrin binding loop #5.

XX  
KW Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;  
KW myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic;  
KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;  
XX inflammatory disorder; angiogenesis; stroke; cerebroprotective.  
OS Unidentified.



XX WO200255344-A2.  
 PN 18-JUL-2002.  
 XX 21-DEC-2001; 2001WO-US049534.  
 XX 23-DEC-2000; 2000US-00747403.  
 PF (DYAX-) DYAX CORP.  
 XX Wescott CR, Beltzer JP, Sato AK;  
 PI WPI; 2002-666875/71.  
 DR Novel synthetic fibrin-binding moiety, useful for detecting, imaging or  
 XX localizing fibrin-containing clots by magnetic resonance imaging,  
 PT radioimaging and for treating diseases involving thrombus formation e.g.  
 PT stroke.  
 XX Claim 4; Page 55; 89pp; English.  
 PS The invention relates to a synthetic fibrin binding group having affinity  
 CC for fibrin. The invention is useful for detecting fibrin in a mammalian  
 CC subject which involves (a) detectably labelling the binding group; (b)  
 CC administering to the subject the labelled polypeptide, and (c) detecting  
 CC the labelled polypeptide in the subject. The invention is useful for  
 CC treating a disease involving thrombus formation eg. deep-vein thrombosis,  
 CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial  
 CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful  
 CC for detection, imaging and localisation of fibrin-containing clots by  
 CC magnetic resonance imaging, radioimaging and other imaging methods and  
 CC are also useful in the diagnosis and treatment of coronary conditions  
 CC where fibrin plays a role. The fibrin binding moieties are useful for  
 CC detecting and diagnosing numerous pathophysiological in which fibrin plays  
 CC a role eg. peritoneal adhesions which often occur after surgery or  
 CC inflammatory and neoplastic processes and are comprised of a fibrin  
 CC network, fibroblasts, macrophages and new blood vessels; rheumatoid  
 CC arthritis, lupus or septic arthritis which often have bits of fibrin  
 CC containing tissues called rice bodies in the synovial fluid of their  
 CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in  
 CC arterioles causes turbulent blood flow resulting in stress and  
 CC destruction of red blood cells. The fibrin specific agents can also be  
 CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain  
 CC or other organs, as well as the detection of tumours, diabetic  
 CC retinopathy, early or high-risk atherosclerosis and other autoimmune and  
 CC inflammatory disorders. Fibrin specific agents also could provide both  
 CC direct or surrogate markers of disease models in which hypoxia and  
 CC angiogenesis are expected to play a role. The invention is also useful  
 CC for screening molecular libraries. The present sequence is a fibrin  
 CC binding loop  
 XX Sequence 9 AA;  
 SQ Query March 100.0%; Score 63; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPGEDWLFC 9  
 DB 1 CPGEDWLFC 9  
 RESULT 2  
 AAE26735  
 ID AAE26735 standard; peptide; 15 AA.  
 XX AAE26735;  
 AC 13-DEC-2002 (first entry)  
 XX Fibrin binding peptide #6.  
 DE Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;  
 XX myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic;  
 KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;  
 KW inflammatory disorder; angiogenesis; stroke; cerebroprotective.  
 XX Unidentified.  
 OS WO200255344-A2.  
 XX 18-JUL-2002.  
 PD 21-DEC-2001; 2001WO-US049534.  
 PF 23-DEC-2000; 2000US-00747403.  
 PR (DYAX-) DYAX CORP.  
 PA Wescott CR, Beltzer JP, Sato AK;  
 XX WPI; 2002-666875/71.  
 DR Novel synthetic fibrin-binding moiety, useful for detecting, imaging or  
 XX localizing fibrin-containing clots by magnetic resonance imaging,  
 PT radioimaging and for treating diseases involving thrombus formation e.g.  
 PT stroke.  
 XX Claim 10; Page 57; 89pp; English.  
 PS The invention relates to a synthetic fibrin binding group having affinity  
 CC for fibrin. The invention is useful for detecting fibrin in a mammalian  
 CC subject which involves (a) detectably labelling the binding group; (b)  
 CC administering to the subject the labelled polypeptide, and (c) detecting  
 CC the labelled polypeptide in the subject. The invention is useful for  
 CC treating a disease involving thrombus formation eg. deep-vein thrombosis,  
 CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial  
 CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful  
 CC for detection, imaging and localisation of fibrin-containing clots by  
 CC magnetic resonance imaging, radioimaging and other imaging methods and  
 CC are also useful in the diagnosis and treatment of coronary conditions  
 CC where fibrin plays a role. The fibrin binding moieties are useful for  
 CC detecting and diagnosing numerous pathophysiological in which fibrin plays

CC a role eg. peritoneal adhesions which often occur after surgery or  
CC inflammatory and neoplastic processes and are comprised of a fibrin  
CC network, fibroblasts, macrophages and new blood vessels; rheumatoid  
CC arthritis, lupus or septic arthritis which often have bits of fibrin  
CC containing tissues called rice bodies in the synovial fluid of their  
CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in  
CC arterioles causes turbulent blood flow resulting in stress and  
CC destruction of red blood cells. The fibrin specific agents can also be  
CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain  
CC or other organs, as well as the detection of tumours, diabetic  
CC retinopathy, early or high-risk atherosclerosis and other autoimmune and  
CC inflammatory disorders. Fibrin specific agents also could provide both  
CC direct or surrogate markers of disease models in which hypoxia and  
CC angiogenesis are expected to play a role. The invention is also useful  
CC for screening molecular libraries. The present sequence is a fibrin  
CC binding peptide  
XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 63; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CPGEDWLCF 9  
Db 4 CPGEDWLCF 12  
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Search completed: May 19, 2004, 17:05:47  
Job time : 39.25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: May 19, 2004, 17:07:54 ; Search time 31.125 Seconds  
(without alignments)  
80.461 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEDWLCF 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues  
Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:  
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17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query %	DB ID	Description
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1 63 100.0 9 14 US-10-034-974-25
2 63 100.0 15 14 US-10-034-974-7
3 51 81.0 9 14 US-10-034-974-49
4 51 81.0 9 14 US-10-034-974-50
5 51 81.0 15 14 US-10-034-974-33
6 51 81.0 15 14 US-10-034-974-34
7 50 79.4 9 14 US-10-034-974-52
8 50 79.4 15 14 US-10-034-974-36
9 48 76.2 9 14 US-10-034-974-46
10 48 76.2 15 14 US-10-034-974-30
11 44 69.8 9 14 US-10-034-974-23
12 44 69.8 15 14 US-10-034-974-5
13 44 69.8 19 14 US-10-034-974-15
14 44 69.8 19 14 US-10-034-974-16
15 44 69.8 19 14 US-10-034-974-17
16 42 66.7 9 14 US-10-034-974-22
17 42 66.7 15 14 US-10-034-974-4
18 42 66.7 147 12 US-10-221-278-286
19 42 66.7 147 15 US-10-291-172-286
20 42 66.7 321 9 US-09-318-271-6
21 42 66.7 455 12 US-10-221-278-662
22 42 66.7 455 15 US-10-291-172-662
23 41 65.1 1222 12 US-10-276-774-2316
24 40 63.5 9 14 US-10-034-974-24
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26 40 63.5 19 14 US-10-034-974-18
27 40 63.5 19 14 US-10-034-974-19
28 40 63.5 19 14 US-10-034-974-20
29 40 63.5 21 10 US-09-880-748-3163
30 40 63.5 21 12 US-10-293-418-3163
31 40 63.5 83 12 US-10-424-599-201051
32 40 63.5 145 12 US-10-424-599-216530
33 40 63.5 190 12 US-10-424-599-257281
34 40 63.5 235 10 US-09-880-748-1914
35 40 63.5 235 12 US-10-293-418-1914
36 40 63.5 481 12 US-10-424-599-158966
37 39 61.9 166 9 US-09-925-301-1076
38 39 61.9 592 15 US-10-369-493-8487
39 38.5 61.1 77 12 US-10-424-599-209980
40 38.5 61.1 513 15 US-10-369-493-2223
41 38 60.3 9 14 US-10-034-974-21
42 38 60.3 9 14 US-10-034-974-53
43 38 60.3 15 14 US-10-034-974-3
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ALIGNMENTS

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; APPLICANT: Beltzer, James P.
; APPLICANT: Westcott, Charles R.
; TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS
; FILE REFERENCE: DYX-024.1 PCT; DYX-024.1 US
; CURRENT APPLICATION NUMBER: US/10/034-974
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 09/747,403
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fibrin binding loop
US-10-034-974-25
Query Match 100.0%; Score 63; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. let06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPGEDWLCF 9
| | | | | | | |
Db 1 CPGEDWLCF 9

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RESULT 2

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US-10-034-974-7
; Sequence 7, Application US/10034974
; Publication No. US20030143158A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Beltzer, James P.
; APPLICANT: Westcott, Charles R.
; APPLICANT: Sato, Aaron K.
; TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS
; FILE REFERENCE: DYX-024.1 PCT; DYX-024.1 US
; CURRENT APPLICATION NUMBER: US/10/034,974
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 09/747,403
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fibrin binding polypeptide
US-10-034-974-7
Query Match 100.0%; Score 63; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CPGEDWLC 9  
DB 4 CPGEDWLC 12

Search completed: May 19, 2004, 17:17:36  
Job time : 32.125 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2004, 16:59:56 ; Search time 10.125 Seconds  
(without alignments)  
85.504 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEDWLC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78: +  
1: pir1: +  
2: pir2: +  
3: pir3: +  
4: pir4: +

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
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3	40	63.5	943	2	S59317	DIP2 protein - yea
4	39	61.9	743	2	C56695	transducin-like en
5	38.5	61.1	513	2	T38770	alpha-amylase a pr
6	38	60.3	271	1	S12516	hypothetical prote
7	38	60.3	279	2	AH2408	permease protein c
8	38	60.3	1035	2	T16588	hypothetical prote
9	37	58.7	137	2	E86251	protein F25C20.8 f
10	37	58.7	144	2	G82092	conserved hypothet
11	37	58.7	262	2	A75009	probable aryl phos
12	37	58.7	388	2	E86239	protein F20524.2 f
13	37	58.7	423	2	G85255	CDP-diacylglycerol

14 37 58.7 423 2 T04915 CDP-diacylglycerol  
15 37 58.7 598 2 S51456 probable membrane  
16 37 58.7 599 2 S67084 probable membrane  
17 37 58.7 626 2 I49100 mscd6 precursor -  
18 37 58.7 1574 2 T13934 MEGF6 protein - ra  
19 37 58.7 2241 2 T16064 hypothetical prote  
20 36.5 57.9 104 2 T49766 hypothetical prote  
21 36.5 57.9 346 2 T1263 xylene monooxygena  
22 36 57.1 99 2 B53116 Ig epsilon chain C  
23 36 57.1 126 2 C53116 Ig epsilon chain C  
24 36 57.1 182 2 D65005 hypothetical prote  
25 36 57.1 182 2 B91030 probable transport  
26 36 57.1 182 2 C65874 probable transport  
27 36 57.1 201 2 S52833 probable heme bind  
28 36 57.1 331 2 T13145 cytosine-specific  
29 36 57.1 388 2 T15075 hypothetical prote  
30 36 57.1 467 2 T19233 hypothetical prote  
31 36 57.1 599 1 H65057 sulfite reductase  
32 36 57.1 599 2 C91081 sulfite reductase  
33 36 57.1 599 2 D85926 fibrinogen alpha c  
34 36 57.1 644 1 FGRUA 3-methyl-2-oxobuta  
35 36 57.1 678 2 G71526 3-methyl-2-oxobuta  
36 36 57.1 678 2 C81683 chloride channel p  
37 36 57.1 805 2 S13410 voltage-gated chor  
38 36 57.1 810 2 S15725 chloride channel p  
39 36 57.1 822 2 S68210 chloride channel p  
40 36 57.1 866 2 D4234 fibrinogen alpha c  
41 36 57.1 889 2 T02240 nitrate reductase  
42 36 57.1 907 2 S23399 chloride channel p  
43 36 57.1 988 2 S37078 chloride channel p  
44 36 57.1 994 2 S15995 chloride channel p  
45 36 57.1 1030 2 I35987 lantibiotic subtil

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OM protein - protein search, using sw model

Run on: May 19, 2004, 16:56:57 ; Search time 7.5 Seconds  
(without alignments)  
62.484 Million cell updates/sec

Title: US-10-034-974-25

Perfect score: 63

Sequence: 1 CPGEDWLC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	66.7	321	1 FCL_HUMAN	Q13630 homo sapien
2	40	63.5	943	1 DIP2_YEAST	Q12220 saccharomyc
3	39	61.9	743	1 TLE2_HUMAN	Q04725 homo sapien
4	39	61.9	767	1 TLE2_MOUSE	Q9wb22 mus musculu
5	38.5	61.1	513	1 AMY3_SCHPO	Q14154 schizosacch
6	38	60.3	321	1 FCL_CRIGR	Q8k3x2 cricetulus
7	38	60.3	321	1 FCL_MOUSE	P23591 mus musculu
8	38	60.3	463	1 ENGA_BIFLO	Q8g6a8 bifidobacte
9	37	58.7	598	1 THI7_YEAST	Q05998 saccharomyc
10	37	58.7	599	1 THI7_YEAST	Q08579 saccharomyc
11	37	58.7	665	1 CD6_MOUSE	Q61003 mus musculu
12	36	57.1	182	1 YFCN_ECOLI	P76938 escherichia
13	36	57.1	201	1 YMW3_YEAST	Q04772 saccharomyc
14	36	57.1	598	1 CRSJ_ECOLI	P38038 escherichia
15	36	57.1	805	1 CICH_TORMA	P21564 torpedo mar
16	36	57.1	809	1 CICH_TORCA	P35522 torpedo cal
17	36	57.1	866	1 FIBA_HUMAN	P02671 homo sapien

18 36 57.1 869 1 N1A3\_MAIZE  
19 36 57.1 898 1 CLC2\_HUMAN  
20 36 57.1 898 1 CLC2\_RABIT  
21 36 57.1 902 1 CLC2\_CAVPO  
22 36 57.1 907 1 CLC2\_RAT  
23 36 57.1 908 1 CLC2\_MOUSE  
24 36 57.1 988 1 CLC1\_HUMAN  
25 36 57.1 994 1 CLC1\_MOUSE  
26 36 57.1 994 1 CLC1\_RAT  
27 36 57.1 1030 1 SPAB\_BAGSU  
28 35 55.6 233 1 YJY5\_YEAST  
29 35 55.6 382 1 N1FV\_RHOCA  
30 35 55.6 670 1 NUSM\_WHEAT  
31 35 55.6 672 1 Y959\_MYCTU  
32 35 55.6 820 1 SYFB\_DEIRA  
33 35 55.6 882 1 HSS1\_HUMAN  
34 35 55.6 882 1 HSS1\_RAT  
35 35 55.6 925 1 NRP2\_RAT  
36 35 55.6 931 1 NRP2\_HUMAN  
37 35 55.6 931 1 NRP2\_MOUSE  
38 35 55.6 2261 1 RRP1\_MUNPEM  
39 34.5 54.8 704 1 MEFB\_MOUSE  
40 34.5 54.8 704 1 MEFB\_RAT  
41 34.5 54.8 1010 1 A1A3\_CHICK  
42 34.5 54.8 1013 1 A1A3\_HUMAN  
43 34.5 54.8 1013 1 A1A3\_RAT  
44 34.5 54.8 1021 1 A1A1\_CHICK  
45 34.5 54.8 1022 1 A1A1\_ANGAN

P49102 zea mays (m  
P51788 homo sapien  
P51789 oryctolagus  
Q9WU45 cavia porce  
P35525 rattus norv  
Q9R0A1 mus musculu  
P35523 homo sapien  
Q64347 mus musculu  
P35524 rattus norv  
P39774 bacillus su  
P39341 saccharomyc  
Q07179 rhodobacter  
Q37680 triticum ae  
P71351 mycobacteri  
Q9RRX5 deinococcus  
P52848 homo sapien  
Q02353 rattus norv  
Q35276 rattus norv  
O60462 homo sapien  
O35375 mus musculu  
P30929 mumps virus  
Q61847 mus musculu  
P28826 rattus norv  
P24798 gallus gall  
P13637 homo sapien  
P06657 rattus norv  
P09572 gallus gall  
Q92030 anguilla an

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OM protein - protein search, using sw model

Run on: May 19, 2004, 16:58:07 ; Search time 27.375 Seconds  
(without alignments)  
103.732 Million cell updates/sec

Title: US-10-034-974-25  
Perfect score: 63  
Sequence: 1 CPGEWMLFC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_25:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_podent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriap:  
17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	45	71.4	1053	16	Q9RK93
2	43	68.3	120	11	Q8C4A2
3	42	66.7	236	16	O67934
4	42	66.7	595	4	Q7Z7K2
5	41	65.1	97	12	Q99D18
6	41	65.1	279	17	Q8TUW3
7	40.5	64.3	1952	5	Q95SN5
8	40.5	64.3	4547	5	Q9W343
9	40	63.5	86	17	Q8TVM2
10	40	63.5	116	5	Q8VMN4
11	40	63.5	183	10	Q8RUL5
12	40	63.5	429	5	Q09538
13	40	63.5	1236	5	Q9NED7
14	39	61.9	196	2	Q8GQ43
15	39	61.9	293	12	Q8QZ69
16	39	61.9	330	3	Q8WZT2
17	39	61.9	482	2	Q8VMJ2
18	39	61.9	548	11	Q8OTG4
19	38	61.9	637	16	Q7WKS9
20	39	61.9	637	16	Q7W8U9
21	39	61.9	2948	4	Q86WG6
22	38.5	61.1	1226	12	Q8JQ07
23	38.5	61.1	1226	12	Q8U206
24	38	60.3	101	17	Q8ZT29
25	38	60.3	157	11	Q8ALH8
26	38	60.3	185	11	Q8BKJ6
27	38	60.3	208	16	Q8ZML6
28	38	60.3	220	10	Q9LKA8
29	38	60.3	279	16	Q8YMW2
30	38	60.3	307	2	Q7X5S1
31	38	60.3	315	16	Q8KYU8
32	38	60.3	321	17	Q8ZU52
33	38	60.3	388	16	Q8IBX5
34	38	60.3	410	12	Q8BDP6
35	38	60.3	463	16	Q8G6A8
36	38	60.3	891	11	Q8B198
37	38	60.3	892	11	Q8B1B7
38	38	60.3	892	11	Q8B167
39	38	60.3	1035	5	Q21380
40	38	60.3	1063	16	Q7U3R7
41	38	60.3	1187	5	Q8WR45
42	37.5	59.5	335	15	O41896
43	37.5	59.5	335	15	Q8ALT8
44	37	58.7	86	2	Q840Q5
45	37	58.7	86	16	Q9R3I9

Q9RK93	streptomyce
Q8C4A2	mus musculus
O67934	acuifex aeo
Q7Z7K2	homo sapien
Q99D18	bovine herp
Q8TUW3	methanopyru
Q95SN5	drosophila
Q9W343	drosophila
Q8TVM2	methanosarc
Q8VMN4	boltenia vi
Q8RUL5	oryza sativ
Q09538	caenorhabdi
Q9NED7	leishmania
Q8GQ43	pseudomonas
Q8QZ69	curcurbit le
Q8WZT2	neurospora
Q8VMJ2	pseudomonas
Q8OTG4	mus musculus
Q7WKS9	bordetella
Q7W8U9	bordetella
Q86WG6	homo sapien
Q8JQ07	rice black
Q8U206	rice black
Q8ZT29	pyrobaculum
Q8ALH8	mus musculus
Q8BKJ6	mus musculus
Q8ZML6	streptomyce
Q9LKA8	arabidopsis
Q8YMW2	anabaena sp
Q7X5S1	enterobacte
Q8KYU8	streptomyce
Q8ZU52	pyrobaculum
Q8IBX5	bacillus ce
Q8BDP6	rubus yello
Q8G6A8	bifidobacte
Q8B198	mus musculus
Q8B1B7	mus musculus
Q8B167	mus musculus
Q21380	caenorhabdi
Q7U3R7	synecococc
Q8WR45	caenorhabdi
O41896	bovine foam
Q8ALT8	bovine foam
Q840Q5	streptomyce
Q9R3I9	streptomyce

Search completed: May 19, 2004, 17:07:48  
Job time : 29.375 secs